CRF Errors Corrected by the STIC System Branch

Serial Number: 07/952,640A

CRF Processing Date: 7/29/93
Edited by: ___
Verified by: DS 7/30/93 (STIC staff)

#14

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Inserted a space between the last nucleic designator and the nucleic number for sequences:

_____

☐ Deleted page numbers in the text of the sequence listing, which is considered invalid text.

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted non-ASCII "garbage" at the end of files, and other invalid text, such as a secretary's initials.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☑ Other: Deleted all hard page break codes

_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

5/26/93

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/07/952,640A*

DATE: 07/29/93
TIME: 14:46:42

INPUT SET: S1104.raw

Au 1806

```
 1                            SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5     (i) APPLICANT: CROWE, JAMES SCOTT
 6                    LEWIS, ALAN PETER
 7
 8    (ii) TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
 9
10   (iii) NUMBER OF SEQUENCES: 46
11
12    (iv) CORRESPONDENCE ADDRESS:
13          (A) ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
14          (B) STREET: 555 THIRTEENTH ST. N.W.
15          (C) CITY: WASHINGTON
16          (D) STATE: D. C.
17          (E) COUNTRY: U.S.
18          (F) ZIP: 20004
19
20     (v) COMPUTER READABLE FORM:
21          (A) MEDIUM TYPE: Floppy disk
22          (B) COMPUTER: IBM PC compatible
23          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26    (vi) CURRENT APPLICATION DATA:
27          (A) APPLICATION NUMBER: US 07/952640
28          (B) FILING DATE: 01-DEC-1992
29          (C) CLASSIFICATION:
30
31  (viii) ATTORNEY/AGENT INFORMATION:
32          (A) NAME: ERNST, BARBARA G
33          (B) REGISTRATION NUMBER: 30,377
34          (C) REFERENCE/DOCKET NUMBER: 1808-118
35
36    (ix) TELECOMMUNICATION INFORMATION:
37          (A) TELEPHONE: (202) 783-6040
38          (B) TELEFAX: (202) 783-6031
39
40
41   (2) INFORMATION FOR SEQ ID NO:1:
42
43     (i) SEQUENCE CHARACTERISTICS:
44          (A) LENGTH: 24 base pairs
45          (B) TYPE: nucleic acid
46          (C) STRANDEDNESS: single
47          (D) TOPOLOGY: linear
48
49    (ii) MOLECULE TYPE: DNA (genomic)
50
51    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
```

Hard page break codes throughout. Delete all. (These don't convert into ASCII appropriately)

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/07/952,640A*

DATE: 07/29/93
TIME: 14:46:44

INPUT SET: S1104.raw

```
52
53      GACATTCAGC TGACCCAGTC TCCA                                    24
54
55      (2) INFORMATION FOR SEQ ID NO:2:
56
57          (i) SEQUENCE CHARACTERISTICS:
58              (A) LENGTH: 24 base pairs
59              (B) TYPE: nucleic acid
60              (C) STRANDEDNESS: single
61              (D) TOPOLOGY: linear
62
63          (ii) MOLECULE TYPE: DNA (genomic)
64
65          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
66
67      GATCAAGCTT CTAACACTCT CCCC                                    24
68
69      (2) INFORMATION FOR SEQ ID NO:3:
70
71          (i) SEQUENCE CHARACTERISTICS:
72              (A) LENGTH: 34 base pairs
73              (B) TYPE: nucleic acid
74              (C) STRANDEDNESS: single
75              (D) TOPOLOGY: linear
76
77          (ii) MOLECULE TYPE: DNA (genomic)
78
79          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
80
81      GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA                         34
82
83      (2) INFORMATION FOR SEQ ID NO:4:
84
85          (i) SEQUENCE CHARACTERISTICS:
86              (A) LENGTH: 16 base pairs
87              (B) TYPE: nucleic acid
88              (C) STRANDEDNESS: single
89              (D) TOPOLOGY: linear
90
91          (ii) MOLECULE TYPE: DNA (genomic)
92
93          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
94
95      AACAGCTATG ACCATG                                             16
96
97      (2) INFORMATION FOR SEQ ID NO:5:
98
99          (i) SEQUENCE CHARACTERISTICS:
100             (A) LENGTH: 17 base pairs
101             (B) TYPE: nucleic acid
102             (C) STRANDEDNESS: single
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/07/952,640A*

```
103              (D)  TOPOLOGY: linear
104
105      (ii)  MOLECULE TYPE: DNA (genomic)
106
107      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:5:
108
109  GTTTTCCCAG TCACGAC                                              17
110
111  (2)  INFORMATION FOR SEQ ID NO:6:
112
113        (i)  SEQUENCE CHARACTERISTICS:
114              (A)  LENGTH: 20 base pairs
115              (B)  TYPE: nucleic acid
116              (C)  STRANDEDNESS: single
117              (D)  TOPOLOGY: linear
118
119      (ii)  MOLECULE TYPE: DNA (genomic)
120
121      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:6:
122
123  GCGTCAGGGT GCTGCTGAGG                                           20
124
125   (2)  INFORMATION FOR SEQ ID NO:7:
126
127        (i)  SEQUENCE CHARACTERISTICS:
128              (A)  LENGTH: 20 base pairs
129              (B)  TYPE: nucleic acid
130              (C)  STRANDEDNESS: single
131              (D)  TOPOLOGY: linear
132
133      (ii)  MOLECULE TYPE: DNA (genomic)
134
135      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:7:
136
137  GGCGGGAAGA TGAAGACAGA                                           20
138
139  (2)  INFORMATION FOR SEQ ID NO:8:
140
141        (i)  SEQUENCE CHARACTERISTICS:
142              (A)  LENGTH: 20 base pairs
143              (B)  TYPE: nucleic acid
144              (C)  STRANDEDNESS: single
145              (D)  TOPOLOGY: linear
146
147      (ii)  MOLECULE TYPE: DNA (genomic)
148
149
150
151      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:8:
152
153  TTCAGCAGGC ACACAACAGA                                           20
```

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/07/952,640A*

DATE: 07/29/93
TIME: 14:46:47

INPUT SET: S1104.raw

```
154
155        (2) INFORMATION FOR SEQ ID NO:9:
156
157            (i) SEQUENCE CHARACTERISTICS:
158                  (A) LENGTH: 1617 base pairs
159                  (B) TYPE: nucleic acid
160                  (C) STRANDEDNESS: both
161                  (D) TOPOLOGY: linear
162
163           (ii) MOLECULE TYPE: cDNA
164
165          (iii) HYPOTHETICAL: NO
166
167           (iv) ANTI-SENSE: NO
168
169
170           (ix) FEATURE:
171                  (A) NAME/KEY: sig_peptide
172                  (B) LOCATION: 35..92
173
174           (ix) FEATURE:
175                  (A) NAME/KEY: mat_peptide
176                  (B) LOCATION: 93..1465
177
178           (ix) FEATURE:
179                  (A) NAME/KEY: CDS
180                  (B) LOCATION: 35..1465
181
182
183           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
184
185  TCTAAAGAAG CCCCTGGGAG CACAGCTCAT CACC ATG GAC TGG ACC TGG AGG          52
186                                         Met Asp Trp Thr Trp Arg
187                                         -19              -15
188
189  TTC CTC TTT GTG GTG GCA GCA GCT ACA GGT GTC CAG TCC CAG ATG CAG        100
190  Phe Leu Phe Val Val Ala Ala Ala Thr Gly Val Gln Ser Gln Met Gln
191          -10                 -5                  1
192
193  GTG GTG CAG TCT GGG GCT GAA GTA AAG AAG CCT GGG TCC TCG GTG ACG        148
194  Val Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Thr
195      5                   10                  15
196
197  GTC TCC TGC AAG GCA TCT GGA GGC ACC TTC AGC AAC TAT GCT ATC AGC        196
198  Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr Ala Ile Ser
199   20                  25                  30                  35
200
201  TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA GGG ATC       244
202  Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile
203                   40                  45                  50
204
```

RAW SEQUENCE LISTING
PATENT APPLICATION   US/07/952,640A

INPUT SET: S1104.raw

```
205   ATC CCT CTT TTT GGT ACA CCA ACC TAC TCA CAG AAC TTC CAG GGC AGA        292
206   Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser Gln Asn Phe Gln Gly Arg
207               55                60                65
208
209   GTC ACG ATT ACC GCG GAC AAA TCC ACC AGC ACA GCC CAC ATG GAG CTG        340
210   Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala His Met Glu Leu
211               70                75                80
212
213   ACT AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT GCG ACA GAT        388
214   Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr Asp
215               85                90                95
216
217   CGC TAC AGG CAG GCA AAT TTT GAC CGG GCC CGG GTT GGC TGG TTC GAC        436
218   Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala Arg Val Gly Trp Phe Asp
219   100               105               110               115·
220
221   CCC TGG GGC CAG GGC ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG        484
222   Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
223               120               125               130
224
225   GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG        532
226   Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
227               135               140               145
228
229   GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG        580
230   Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
231               150               155               160
232
233   GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC        628
234   Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
235               165               170               175
236
237   TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG        676
238   Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
239   180               185               190               195
240
241   GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC AAC        724
242   Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
243               200               205               210
244
245   GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC        772
246   Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
247               215               220               225
248
249   AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA        820
250   Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
251               230               235               240
252
253   CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC        868
254   Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
255               245               250               255
```

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256
257   ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC      916
258   Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
259   260             265             270             275
260
261    GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC      964
262   Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
263               280             285             290
264
265   GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC     1012
266   Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
267               295             300             305
268
269   AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG     1060
270   Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
271           310             315             320
272
273   CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA     1108
274   Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
275       325             330             335
276
277   GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA     1156
278   Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
279   340             345             350             355
280
281   CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC     1204
282   Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
283               360             365             370
284
285   CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC     1252
286   Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
287               375             380             385
288
289   GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC     1300
290   Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
291           390             395             400
292
293   ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG     1348
294   Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
295       405             410             415
296
297   CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC     1396
298   Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
299   420             425             430             435
300
301   TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC     1444
302   Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
303               440             445             450
304
305   TCC CTG TCT CCG GGT AAA TGAGTGCGAC GGCCGGCAAG CCCCCGCTCC     1492
306   Ser Leu Ser Pro Gly Lys
```

```
307                  455
308
309   CCGGGCTCTC GCGGTCGCAC GAGGATGCTT GGCACGTACC CCGTGTACAT ACTTCCCGGG    1552
310
311   CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAAA AAAAAAAAAA    1612
312
313   AAAAA                                                                1617
314      (2) INFORMATION FOR SEQ ID NO:10:
315
316         (i) SEQUENCE CHARACTERISTICS:
317             (A) LENGTH: 476 amino acids
318             (B) TYPE: amino acid
319             (D) TOPOLOGY: linear
320
321         (ii) MOLECULE TYPE: protein
322
323         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
324
325   Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
326   -19             -15                 -10                 -5
327
328   Val Gln Ser Gln Met Gln Val Val Gln Ser Gly Ala Glu Val Lys Lys
329                    1               5                 10
330
331   Pro Gly Ser Ser Val Thr Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
332        15                 20                 25
333
334   Ser Asn Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
335    30                 35                 40                 45
336
337   Glu Trp Met Gly Gly Ile Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser
338                 50                 55                 60
339
340   Gln Asn Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
341                 65                 70                 75
342
343   Thr Ala His Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val
344             80                 85                 90
345
346   Tyr Tyr Cys Ala Thr Asp Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala
347        95                 100                105
348
349   Arg Val Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
350   110             115                120                125
351
352   Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
353                 130                135                140
354
355   Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
356             145                150                155
357
```

INPUT SET: S1104.raw

```
358    Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
359            160             165             170
360
361    Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
362            175             180             185
363
364    Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
365    190             195             200             205
366
367     Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
368                210             215             220
369
370    Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
371            225             230             235
372
373    Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
374            240             245             250
375
376    Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
377            255             260             265
378
379    Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
380    270             275             280             285
381
382    Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
383                290             295             300
384
385    Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
386            305             310             315
387
388    Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
389            320             325             330
390
391    Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
392            335             340             345
393
394    Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
395    350             355             360             365
396
397    Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
398            370             375             380
399
400    Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
401            385             390             395
402
403    Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
404            400             405             410
405
406    Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
407            415             420             425
408
```

```
409  Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
410  430             435             440                 445
411
412  Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
413              450             455
414
415
416     (2) INFORMATION FOR SEQ ID NO:11:
417
418         (i) SEQUENCE CHARACTERISTICS:
419             (A) LENGTH: 902 base pairs
420             (B) TYPE: nucleic acid
421             (C) STRANDEDNESS: both
422             (D) TOPOLOGY: linear
423
424        (ii) MOLECULE TYPE: cDNA
425
426       (iii) HYPOTHETICAL: NO
427
428        (iv) ANTI-SENSE: NO
429
430
431        (ix) FEATURE:
432             (A) NAME/KEY: CDS
433             (B) LOCATION: 32..739
434
435        (ix) FEATURE:
436             (A) NAME/KEY: mat_peptide
437             (B) LOCATION: 89..739
438
439        (ix) FEATURE:
440             (A) NAME/KEY: sig_peptide
441             (B) LOCATION: 32..86
442
443
444        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
445
446  CAAGAGGCAG CGCTCTCGGG ACGTCTCCAC C ATG GCC TGG GCT CTG CTG CTC      52
447                                    Met Ala Trp Ala Leu Leu Leu
448                                    -19             -15
449
450  CTC ACC CTC CTC ACT CAG GAC ACA GGG TCC TGG GCC CAG TCT GCC CTG     100
451  Leu Thr Leu Leu Thr Gln Asp Thr Gly Ser Trp Ala Gln Ser Ala Leu
452          -10             -5                  1
453
454  ACT CAG CCT GCC TCC GTG TCT GGG TCT CCT GGA CAG TCG ATC ACC ATC     148
455  Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile
456   5               10                  15                  20
457
458  TCC TGC ACT GGA ACC AAC AAT GAT GTT GGG AGT TAT AAC CTT GTC TCC     196
459  Ser Cys Thr Gly Thr Asn Asn Asp Val Gly Ser Tyr Asn Leu Val Ser
```

INPUT SET: S1104.raw

```
460                            25                      30                      35
461
462     TGG TAC CAG CAG CAC CCA GGC AAA GCC CCC AAA ATC ATG ATT TAT GAG          244
463     Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Ile Met Ile Tyr Glu
464                            40                      45                      50
465
466     GTC AGT AAG CGG CCC TCA GGG GTT TCT AAT CGC TTC TCT GGC TCC AAG          292
467     Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys
468                            55                      60                      65
469
470     TCT GGC AAC ACG GCC TCC CTG ACA ATC TCT GGG CTC CAG GCT GAG GAC          340
471     Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp
472                            70                      75                      80
473
474     GAG GCT GAT TAT TAC TGC TGC TCA TAT GCA GGT AGT TAC ACT GTG GTT          388
475     Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser Tyr Thr Val Val
476         85                          90                      95                    100
477
478     TTC GGC GGA GGG ACC AAA CTG ACC GTC CTA GGT CAG CCC AAG GCT GCC          436
479     Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
480                            105                     110                     115
481
482     CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG CTT CAA GCC AAC          484
483     Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
484                            120                     125                     130
485
486     AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG          532
487     Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
488                            135                     140                     145
489
490     ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG          580
491     Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
492             150                         155                     160
493
494     ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC          628
495     Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
496     165                        170                     175                     180
497
498     TAT CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC          676
499     Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
500                            185                     190                     195
501
502     TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT          724
503     Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
504                            200                     205                     210
505
506     ACA GAA TGT TCA TAGGTTCTAA ACCCTCACCC CCCCCACGGG AGACTAGAGC             776
507     Thr Glu Cys Ser
508                 215
509
510     TGCAGGATCC CAGGGGAGGG GTCTCTCCTC CCACCCCAAG GCATCAAGCC CTTCTCCCTG        836
```

PAGE: 11

RAW SEQUENCE LISTING
PATENT APPLICATION *US/07/952,640A*

DATE: 07/29/93
TIME: 14:47:28

INPUT SET: S1104.raw

```
511
512    CACTCAATAA ACCCTCAATA AATATTCTCA TTGTCAATCA CAAAAAAAAA AAAAAAAAA         896
513
514    AAAAAA                                                                   902
515
516
517    (2) INFORMATION FOR SEQ ID NO:12:
518
519            (i) SEQUENCE CHARACTERISTICS:
520                    (A) LENGTH: 235 amino acids
521                    (B) TYPE: amino acid
522                    (D) TOPOLOGY: linear
523
524            (ii) MOLECULE TYPE: protein
525
526            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
527
528    Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr Gly
529    -19              -15              -10              -5
530
531    Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
532              1              5              10
533
534    Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Asn Asn Asp Val
535         15              20              25
536
537    Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
538    30              35              40              45
539
540    Pro Lys Ile Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser
541              50              55              60
542
543    Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
544              65              70              75
545
546    Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
547              80              85              90
548
549    Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
550              95              100              105
551
552    Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
553    110              115              120              125
554
555    Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
556              130              135              140
557
558    Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
559              145              150              155
560
561    Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
```

```
562                160                 165                 170
563
564   Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
565        175                 180                 185
566
567   Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
568   190                 195                 200                 205
569
570   Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
571                210                 215      (2) INFORMATION FOR SEQ ID NO:13:
572
573        (i) SEQUENCE CHARACTERISTICS:
574            (A) LENGTH: 321 base pairs
575            (B) TYPE: nucleic acid
576            (C) STRANDEDNESS: both
577            (D) TOPOLOGY: linear
578
579       (ii) MOLECULE TYPE: cDNA
580
581      (iii) HYPOTHETICAL: NO
582
583       (iv) ANTI-SENSE: NO
584
585
586       (ix) FEATURE:
587            (A) NAME/KEY: CDS
588            (B) LOCATION: 1..321
589
590
591       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
592
593   GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA        48
594   Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
595    1               5                  10                  15
596
597   GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT        96
598   Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
599            20                  25                  30
600
601   TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC       144
602   Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
603            35                  40                  45
604
605   TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC ACA TCA AGG TTC AGT GGC       192
606   Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
607            50                  55                  60
608
609   AGT GGA TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT       240
610   Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
611    65                  70                  75                  80
612
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INPUT SET: S1104.raw

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613     GAA GAT TCT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG ATC          288
614     Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
615                     85                  90                  95
616
617     ACC TTC GGC CAA GGG ACA CGA CTG GAG ATT AAA                              321
618     Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
619                     100                 105
620
621
622     (2) INFORMATION FOR SEQ ID NO:14:
623
624             (i) SEQUENCE CHARACTERISTICS:
625                     (A) LENGTH: 107 amino acids
626                     (B) TYPE: amino acid
627                     (D) TOPOLOGY: linear
628
629         (ii) MOLECULE TYPE: protein
630
631         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
632
633     Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
634      1              5                  10                  15
635
636     Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
637                     20                  25                  30
638
639     Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
640             35                  40                  45
641
642     Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
643         50                  55                  60
644
645     Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
646      65                  70                  75                  80
647
648     Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
649                     85                  90                  95
650
651     Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
652                     100                 105
653
654     (2) INFORMATION FOR SEQ ID NO:15:
655
656             (i) SEQUENCE CHARACTERISTICS:
657                     (A) LENGTH: 324 base pairs
658                     (B) TYPE: nucleic acid
659                     (C) STRANDEDNESS: both
660                     (D) TOPOLOGY: linear
661
662         (ii) MOLECULE TYPE: cDNA
663
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/07/952,640A*

DATE: 07/29/93
TIME: 14:47:49

INPUT SET: S1104.raw

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664      (iii) HYPOTHETICAL: NO
665
666      (iv) ANTI-SENSE: NO
667
668
669      (ix) FEATURE:
670           (A) NAME/KEY: CDS
671           (B) LOCATION: 1..324
672
673
674      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
675
676  GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA      48
677  Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
678   1               5                  10                  15
679
680  GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT      96
681  Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
682               20                  25                  30
683
684  TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT GAG CTC CTG ATC     144
685  Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
686           35                  40                  45
687
688  TAT GCT GCT TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC     192
689  Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
690       50                  55                  60
691
692  AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT     240
693  Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
694   65                  70                  75                  80
695
696  GAA GAT TCT GCA GTT TAT TAC TGT CAA CAC ACT TAT AGT GAC CCG TAC     288
697  Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
698               85                  90                  95
699
700  AGT TTT GGC CAG GGG ACC AAA GTG GAC ATC AAA CGA                     324
701  Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
702               100                 105
703
704
705  (2) INFORMATION FOR SEQ ID NO:16:
706
707      (i) SEQUENCE CHARACTERISTICS:
708           (A) LENGTH: 108 amino acids
709           (B) TYPE: amino acid
710           (D) TOPOLOGY: linear
711
712      (ii) MOLECULE TYPE: protein
713
714      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/07/952,640A*

DATE: 07/29/93
TIME: 14:47:55

INPUT SET: S1104.raw

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715
716    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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718
719    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
720             20                  25                  30
721
722    Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
723         35                  40                  45
724
725    Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
726         50                  55                  60
727
728    Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
729     65                  70                  75                  80
730
731    Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
732                 85                  90                  95
733
734    Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
735             100                 105
736
737    (2)  INFORMATION FOR SEQ ID NO:17:
738
739        (i)  SEQUENCE CHARACTERISTICS:
740            (A)  LENGTH: 324 base pairs
741            (B)  TYPE: nucleic acid
742            (C)  STRANDEDNESS: both
743            (D)  TOPOLOGY: linear
744
745       (ii)  MOLECULE TYPE: cDNA
746
747      (iii)  HYPOTHETICAL: NO
748
749       (iv)  ANTI-SENSE: NO
750
751
752       (ix)  FEATURE:
753            (A)  NAME/KEY: CDS
754            (B)  LOCATION: 1..324
755
756
757       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:17:
758
759    GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCT TCT GTA GGA        48
760    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
761  ·  1               5                  10                  15
762
763    GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGC ACT TAT        96
764    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
765             20                  25                  30
```

```
766
767   TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC          144
768   Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
769            35                  40                  45
770
771   TAT TAT GCA AAC AGT TTG GCA AGT GGG GTC CCA TCA AGG TTC AGC GGC          192
772   Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
773            50                  55                  60
774
775   AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT          240
776   Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
777   65                  70                  75                  80
778
779   GAA GAT TCT GCA ACT TAT TAC TGT GGA CAG GGT AAT AGT TAC CCT CTC          288
780   Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu
781                  85                  90                  95
782
783   ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                          324
784   Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
785            100                 105
786
787
788   (2)  INFORMATION FOR SEQ ID NO:18:
789
790          (i)  SEQUENCE CHARACTERISTICS:
791                 (A)  LENGTH: 108 amino acids
792                 (B)  TYPE: amino acid
793                 (D)  TOPOLOGY: linear
794
795         (ii)  MOLECULE TYPE: protein
796
797         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:18:
798
799   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
800    1               5                  10                  15
801
802   Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
803            20                  25                  30
804
805   Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
806            35                  40                  45
807
808   Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
809            50                  55                  60
810
811   Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
812   65                  70                  75                  80
813
814   Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu
815                  85                  90                  95
816
```

```
817    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
818              100                 105
819
820    (2) INFORMATION FOR SEQ ID NO:19:
821
822        (i) SEQUENCE CHARACTERISTICS:
823             (A) LENGTH: 324 base pairs
824             (B) TYPE: nucleic acid
825             (C) STRANDEDNESS: both
826             (D) TOPOLOGY: linear
827
828       (ii) MOLECULE TYPE: cDNA
829
830      (iii) HYPOTHETICAL: NO
831
832       (iv) ANTI-SENSE: NO
833
834
835       (ix) FEATURE:
836             (A) NAME/KEY: CDS
837             (B) LOCATION: 1..324
838
839
840       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
841
842    GAC ATT CAG CTG ACC CAG TCT CCA TCC TCT CAG TCT GCA TCT GTA GGA        48
843    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly
844     1                5                 10                  15
845
846    GAC AGA GTG ACC ATT ACT TGC CAG GCG AGT CAA AGC CTT AGC AAT TAT        96
847    Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr
848              20                  25                  30
849
850    TTA AAT TGG TAT CAG CAG AAA CCA GGG AAA ATT CCT AAG CTC CTG ATC       144
851    Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
852              35                  40                  45
853
854    TAT AGG GCA TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC       192
855    Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
856         50                  55                  60
857
858    AGT GGA TCT GGG ACG GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
859    Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
860     65                  70                  75                  80
861
862    GAA GAT TTT GCC ACT TAT TAC TGT CAG CAT AAT TAT GGT ACC CCT CTC       288
863    Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu
864                  85                  90                  95
865
866    ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                       324
867    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
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RAW SEQUENCE LISTING
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DATE: 07/29/93
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INPUT SET: S1104.raw

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868                     100                     105
869
870
871     (2) INFORMATION FOR SEQ ID NO:20:
872
873           (i) SEQUENCE CHARACTERISTICS:
874                 (A) LENGTH: 108 amino acids
875                 (B) TYPE: amino acid
876                 (D) TOPOLOGY: linear
877
878         (ii) MOLECULE TYPE: protein
879
880         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
881
882     Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly
883      1               5                  10                  15
884
885     Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr
886              20                      25                  30
887
888     Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
889          35                      40                  45
890
891     Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
892          50                  55                  60
893
894     Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
895      65                  70                  75                  80
896
897     Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu
898              85                      90                  95
899
900     Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
901              100                     105
902
903     (2) INFORMATION FOR SEQ ID NO:21:
904
905           (i) SEQUENCE CHARACTERISTICS:
906                 (A) LENGTH: 324 base pairs
907                 (B) TYPE: nucleic acid
908                 (C) STRANDEDNESS: both
909                 (D) TOPOLOGY: linear
910
911         (ii) MOLECULE TYPE: DNA (genomic)
912
913
914         (ix) FEATURE:
915                 (A) NAME/KEY: CDS
916                 (B) LOCATION: 1..324
917
918         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
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RAW SEQUENCE LISTING
PATENT APPLICATION US/07/952,640A

INPUT SET: S1104.raw

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919
920     GACATTCAGC TGACCCAGTC TCCACTCTCC CTGCCCGTCA GTCTTGGAGA GTCGGCCTCC        60
921
922     ATCTCCTNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN       120
923
924     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNTCCCAGAC       180
925
926     AGGTTCACTG GCAGTGGGTC AGGCACTGAT TTCACACTGA AAATCAGCAG AGTGGAGGCT       240
927
928     GAGGATGTTG GGGTTTATTA CTGCATGCAA GCTCTTCGGT CTCCTTGGAC GTTCGGCCAA       300
929
930     GGGACCAAGG TGGAAATCAG ACGA                                             324
931
932
933     (2)  INFORMATION FOR SEQ ID NO:22:
934
935          (i)  SEQUENCE CHARACTERISTICS:
936               (A)  LENGTH: 108 amino acids
937               (B)  TYPE: amino acid
938               (D)  TOPOLOGY: linear
939
940          (ii) MOLECULE TYPE: protein
941
942          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
943
944          Asp Ile Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
945          1               5                   10                  15
946
947          Glu Ser Ala Ser Ile Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
948                       20              25                  30
949
950          Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
951                   35                  40                  45
952
953          Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asp Arg Phe Thr Gly
954               50                  55                  60
955
956          Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
957          65                  70                  75                  80
958
959          Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Arg Ser Pro Trp
960                           85                  90                  95
961
962          Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg Arg
963                       100                 105
964
965     (2)  INFORMATION FOR SEQ ID NO:23:
966
967          (i)  SEQUENCE CHARACTERISTICS:
968               (A)  LENGTH: 324 base pairs
969               (B)  TYPE: nucleic acid
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970                    (C)  STRANDEDNESS: both
971                    (D)  TOPOLOGY: linear
972
973            (ii)  MOLECULE TYPE: cDNA
974
975           (iii)  HYPOTHETICAL: NO
976
977            (iv)  ANTI-SENSE: NO
978
979
980            (ix)  FEATURE:
981                    (A)  NAME/KEY: CDS
982                    (B)  LOCATION: 1..324
983
984
985            (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:23:
986
987    GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA          48
988    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
989     1               5                   10                  15
990
991    GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT          96
992    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
993                20                  25                  30
994
995    TTA AGT TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CTC CTG ATC         144
996    Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
997                35                  40                  45
998
999    TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC         192
1000   Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1001        50                  55                  60
1002
1003   AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAA CCT         240
1004   Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1005    65                  70                  75                  80
1006
1007   GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG GGT TAT GGT ACC CCG TAC         288
1008   Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
1009                85                  90                  95
1010
1011   AGT TTT GGC CAG GGG ACC AAA GTG GAG ATC AAA CGA                         324
1012   Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1013                100                 105
1014
1015
1016    (2)  INFORMATION FOR SEQ ID NO:24:
1017
1018            (i)  SEQUENCE CHARACTERISTICS:
1019                    (A)  LENGTH: 108 amino acids
1020                    (B)  TYPE: amino acid
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RAW SEQUENCE LISTING
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1021                    (D)  TOPOLOGY:  linear
1022
1023          (ii)  MOLECULE TYPE:  protein
1024
1025          (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:24:
1026
1027     Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1028      1               5                  10                  15
1029
1030     Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
1031              20                  25                  30
1032
1033     Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1034              35                  40                  45
1035
1036     Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1037          50                  55                  60
1038
1039     Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1040      65                  70                  75                  80
1041
1042     Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
1043                  85                  90                  95
1044
1045     Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1046              100                 105
1047
1048     (2)  INFORMATION FOR SEQ ID NO:25:
1049
1050          (i)  SEQUENCE CHARACTERISTICS:
1051               (A)  LENGTH:  324 base pairs
1052               (B)  TYPE:  nucleic acid
1053               (C)  STRANDEDNESS:  both
1054               (D)  TOPOLOGY:  linear
1055
1056          (ii)  MOLECULE TYPE:  cDNA
1057
1058         (iii)  HYPOTHETICAL:  NO
1059
1060          (iv)  ANTI-SENSE:  NO
1061
1062
1063          (ix)  FEATURE:
1064               (A)  NAME/KEY:  CDS
1065               (B)  LOCATION:  1..324
1066
1067
1068          (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:25:
1069
1070     GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA          48
1071     Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
```

```
1072     1               5                   10                   15
1073
1074     GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GAC ATT AGC AAT AAT        96
1075     Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
1076                 20                  25                  30
1077
1078     TTA GTC TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC       144
1079     Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1080                 35                  40                  45
1081
1082     TAT GCT GCA TCC AGA TTG CAA GAT GGG GTC CCA TCA AGG TTC AGC GGC       192
1083     Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
1084                 50                  55                  60
1085
1086     AGT GGG TCT GGG ACC GAT TTC ACC CTC ACA ATT AAT CCT GTG GAA GCT       240
1087     Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
1088     65                  70                  75                  80
1089
1090     GAC GAT GCT GCG GAT TAC TAC TGT CTA CAG ACT AAG AGT TCT CCT CGG       288
1091     Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg
1092                 85                  90                  95
1093
1094     ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGA                       324
1095     Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1096                 100                 105
1097
1098
1099     (2) INFORMATION FOR SEQ ID NO:26:
1100
1101         (i) SEQUENCE CHARACTERISTICS:
1102             (A) LENGTH: 108 amino acids
1103             (B) TYPE: amino acid
1104             (D) TOPOLOGY: linear
1105
1106         (ii) MOLECULE TYPE: protein
1107
1108         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
1109
1110     Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1111     1               5                   10                  15
1112
1113     Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
1114                 20                  25                  30
1115
1116     Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1117                 35                  40                  45
1118
1119     Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
1120                 50                  55                  60
1121
1122     Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
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PATENT APPLICATION   *US/07/952,640A*

DATE: 07/29/93
TIME: 14:48:50

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1123     65                  70                 75                 80
1124
1125   Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg
1126                  85                 90                 95
1127
1128   Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1129              100                 105
1130
1131   (2) INFORMATION FOR SEQ ID NO:27:
1132
1133       (i) SEQUENCE CHARACTERISTICS:
1134           (A) LENGTH: 324 base pairs
1135           (B) TYPE: nucleic acid
1136           (C) STRANDEDNESS: both
1137           (D) TOPOLOGY: linear
1138
1139      (ii) MOLECULE TYPE: DNA (genomic)
1140
1141
1142      (ix) FEATURE:
1143           (A) NAME/KEY: CDS
1144           (B) LOCATION: 1..324
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1146      (ix) FEATURE:
1147           (A) NAME/KEY: mat_peptide
1148           (B) LOCATION: 31..324
1149
1150
1151      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
1152
1153   GACATTCAGC TGACCCAGTC TCCANNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN      60
1154
1155   NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN     120
1156
1157   NNNNNNNNNN NNCAGCCCTT GATTTATGAG GTTTCCAACC GGGCCTCTGG AGTCCCAGAC     180
1158
1159   AGGTTCAGTG GCAGTGGGTC GGACACTGAT TTCACACTCA AAATCAGCAG AGTGGAGGCT     240
1160
1161   GAGGATGTTG GGGTTTATTA CTGCATGCAA TATACACACA TTCCATTCAC TTTCGGCCCC     300
1162
1163   GGGACCAAAC TGGATATCAA ACGA                                           324
1164
1165   (2) INFORMATION FOR SEQ ID NO:28:
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1167       (i) SEQUENCE CHARACTERISTICS:
1168           (A) LENGTH: 108 amino acids
1169           (B) TYPE: amino acid
1170           (D) TOPOLOGY: linear
1171
1172      (ii) MOLECULE TYPE: protein
1173
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1174
1175
1176        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:28:
1177
1178        Asp Ile Gln Leu Thr Gln Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1179        1               5                   10                  15
1180
1181        Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1182                    20                  25                  30
1183
1184        Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Pro Leu Ile
1185                    35                  40                  45
1186
1187        Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1188            50                  55                  60
1189
1190        Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1191        65                  70                  75                  80
1192
1193        Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1194                    85                  90                  95
1195
1196        Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1197                    100                 105
1198
1199
1200
1201
1202    (2)  INFORMATION FOR SEQ ID NO:29:
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1204        (i)  SEQUENCE CHARACTERISTICS:
1205             (A)  LENGTH: 324 base pairs
1206             (B)  TYPE: nucleic acid
1207             (C)  STRANDEDNESS: both
1208             (D)  TOPOLOGY: linear
1209
1210        (ii)  MOLECULE TYPE: cDNA
1211
1212        (iii)  HYPOTHETICAL: NO
1213
1214        (iv)  ANTI-SENSE: NO
1215
1216
1217        (ix)  FEATURE:
1218             (A)  NAME/KEY: CDS
1219             (B)  LOCATION: 1..324
1220
1221
1222        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:29:
1223
1224    GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA          48
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1225    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1226    1               5                   10                  15
1227
1228    GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT        96
1229    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
1230                20                  25                  30
1231
1232    TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT CAG CCC TTG ATT       144
1233    Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile
1234            35                  40                  45
1235
1236    TAT GAG GTT TCC AAC CGG GCC TCT GGA GTC CCA GAC AGG TTC AGT GGC       192
1237    Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1238        50                  55                  60
1239
1240    AGT GGG TCG GAC ACT GAT TTC ACA CTC AAA ATC AGC AGA GTG GAG GCT       240
1241    Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1242    65                  70                  75                  80
1243
1244    GAG GAT GTT GGG GTT TAT TAC TGC ATG CAA TAT ACA CAC ATT CCA TTC       288
1245    Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1246                85                  90                  95
1247
1248    ACT TTC GGC CCC GGG ACC AAA CTG GAT ATC AAA CGA                       324
1249    Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1250                100                 105
1251
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1253    (2) INFORMATION FOR SEQ ID NO:30:
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1255        (i) SEQUENCE CHARACTERISTICS:
1256            (A) LENGTH: 108 amino acids
1257            (B) TYPE: amino acid
1258            (D) TOPOLOGY: linear
1259
1260        (ii) MOLECULE TYPE: protein
1261
1262        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30
1263
1264    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1265    1               5                   10                  15
1266
1267    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
1268                20                  25                  30
1269
1270    Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile
1271            35                  40                  45
1272
1273    Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1274        50                  55                  60
1275
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RAW SEQUENCE LISTING
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INPUT SET: S1104.raw

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1276    Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1277     65              70              75                      80
1278
1279    Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1280             85                  90                      95
1281
1282    Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1283            100             105
1284
1285    (2)  INFORMATION FOR SEQ ID NO:31
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1287        (i)  SEQUENCE CHARACTERISTICS:
1288             (A)  LENGTH: 324 base pairs
1289             (B)  TYPE: nucleic acid
1290             (C)  STRANDEDNESS: both
1291             (D)  TOPOLOGY: linear
1292
1293       (ii)  MOLECULE TYPE: cDNA
1294
1295      (iii)  HYPOTHETICAL: NO
1296
1297       (iv)  ANTI-SENSE: NO
1298
1299
1300       (ix)  FEATURE:
1301             (A)  NAME/KEY: CDS
1302             (B)  LOCATION: 1..324
1303
1304
1305       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:31
1306
1307    GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA        48
1308    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1309     1               5                  10                      15
1310
1311    GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GGC ATT AGC AAT AAT        96
1312    Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1313             20                  25                      30
1314
1315    TTA GCC TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CGC CTG ATC       144
1316    Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1317             35                  40                      45
1318
1319    TAT GCT GCA TCC AGT TTG GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC       192
1320    Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1321         50                  55                  60
1322
1323    AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
1324    Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1325     65              70                  75                      80
1326
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1327   GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG GAT AAC AGT TAT CCT TTC        288
1328   Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1329                   85              90                      95
1330
1331   ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                        324
1332   Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1333                   100                 105
1334
1335
1336      (2) INFORMATION FOR SEQ ID NO:32
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1338          (i)  SEQUENCE CHARACTERISTICS:
1339               (A) LENGTH: 108 amino acids
1340               (B) TYPE: amino acid
1341               (D) TOPOLOGY: linear
1342
1343         (ii) MOLECULE TYPE: protein
1344
1345         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32
1346
1347   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1348    1               5                  10                  15
1349
1350   Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1351                   20                  25                  30
1352
1353   Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1354               35                  40                  45
1355
1356   Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1357           50                  55                  60
1358
1359   Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1360   65                  70                  75                  80
1361
1362   Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1363                   85                  90                  95
1364
1365   Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1366                   100                 105
1367
1368      (2) INFORMATION FOR SEQ ID NO:33
1369
1370          (i)  SEQUENCE CHARACTERISTICS:
1371               (A) LENGTH: 324 base pairs
1372               (B) TYPE: nucleic acid
1373               (C) STRANDEDNESS: both
1374               (D) TOPOLOGY: linear
1375
1376         (ii) MOLECULE TYPE: cDNA
1377
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INPUT SET: S1104.raw

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1378        (iii) HYPOTHETICAL: NO
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1380        (iv) ANTI-SENSE: NO
1381
1382
1383        (ix) FEATURE:
1384             (A) NAME/KEY: CDS
1385             (B) LOCATION: 1..324
1386
1387
1388        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33
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1390    GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA        48
1391    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1392     1               5                  10                  15
1393
1394    GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GGC ATT AGC AAT AAT        96
1395    Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1396                20                  25                  30
1397
1398    TTA GCC TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CGC CTG ATC       144
1399    Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1400                35                  40                  45
1401
1402    TAT GCT GCA TCC AGT TTG GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC       192
1403    Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1404            50                  55                  60
1405
1406    AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
1407    Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1408     65                  70                  75                  80
1409
1410    GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG GAT AAC AGT TAT CCT TTC       288
1411    Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1412                85                  90                  95
1413
1414    ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                       324
1415    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1416                100                 105
1417
1418
1419    (2) INFORMATION FOR SEQ ID NO:34
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1421             (i) SEQUENCE CHARACTERISTICS:
1422                 (A) LENGTH: 108 amino acids
1423                 (B) TYPE: amino acid
1424                 (D) TOPOLOGY: linear
1425
1426             (ii) MOLECULE TYPE: protein
1427
1428             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/07/952,640A*
DATE: 07/29/93
TIME: 14:49:31

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1429
1430    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1431     1               5                  10                  15
1432
1433    Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1434             20                  25                  30
1435
1436    Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1437             35                  40                  45
1438
1439    Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1440         50                  55                  60
1441
1442    Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1443     65                  70                  75                  80
1444
1445    Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1446                 85                  90                  95
1447
1448    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1449             100                 105
1450
1451    (2) INFORMATION FOR SEQ ID NO:35:
1452
1453        (i) SEQUENCE CHARACTERISTICS:
1454            (A) LENGTH: 342 base pairs
1455            (B) TYPE: nucleic acid
1456            (C) STRANDEDNESS: both
1457            (D) TOPOLOGY: linear
1458
1459        (ii) MOLECULE TYPE: cDNA
1460
1461
1462        (ix) FEATURE:
1463            (A) NAME/KEY: CDS
1464            (B) LOCATION: 1..342
1465
1466
1467        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
1468
1469    GAC ATT GTG ATG ACT CAG TCT CCA ACT TTC CTT GCT GTG ACA GCA AGT        48
1470    Asp Ile Val Met Thr Gln Ser Pro Thr Phe Leu Ala Val Thr Ala Ser
1471     1               5                  10                  15
1472
1473    AAG AAG GTC ACC ATT AGT TGC ACT GCC TCT GAG AGC CTT TAT TCA AGC        96
1474    Lys Lys Val Thr Ile Ser Cys Thr Ala Ser Glu Ser Leu Tyr Ser Ser
1475             20                  25                  30
1476
1477    AAA CAC AAG GTG CAC TAC TTG GCT TGG TAC CAG AAG AAA CCA GAG CAA       144
1478    Lys His Lys Val His Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Glu Gln
1479             35                  40                  45
```

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1480
1481    TCT CCT AAA CTG CTG ATA TAC GGG GCA TCC AAC CGA TAC ATT GGG GTC          192
1482    Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Ile Gly Val
1483         50                      55                      60
1484
1485    CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTG ACC          240
1486    Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1487    65                      70                      75                  80
1488
1489    ATC AGC AGT GTA CAG GTT GAA GAC CTC ACA CAT TAT TAC TGT GCA CAG          288
1490    Ile Ser Ser Val Gln Val Glu Asp Leu Thr His Tyr Tyr Cys Ala Gln
1491                        85                      90                  95
1492
1493    TTT TAC AGC TAT CCT CTC ACG TTC GGT GCT GGG ACC AAG CTG GAG CTG          336
1494    Phe Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
1495                        100                     105                 110
1496
1497    AAA CGG                                                                  342
1498    Lys Arg
1499
1500
1501
1502    (2)  INFORMATION FOR SEQ ID NO:36:
1503
1504         (i)  SEQUENCE CHARACTERISTICS:
1505              (A) LENGTH: 114 amino acids
1506              (B) TYPE: amino acid
1507              (D) TOPOLOGY: linear
1508
1509         (ii) MOLECULE TYPE: protein
1510
1511         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
1512
1513    Asp Ile Val Met Thr Gln Ser Pro Thr Phe Leu Ala Val Thr Ala Ser
1514     1               5                      10                      15
1515
1516    Lys Lys Val Thr Ile Ser Cys Thr Ala Ser Glu Ser Leu Tyr Ser Ser
1517                20                      25                      30
1518
1519    Lys His Lys Val His Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Glu Gln
1520                35                      40                      45
1521
1522    Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Ile Gly Val
1523         50                      55                      60
1524
1525    Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1526    65                      70                      75                  80
1527
1528    Ile Ser Ser Val Gln Val Glu Asp Leu Thr His Tyr Tyr Cys Ala Gln
1529                        85                      90                  95
1530
```

```
1531   Phe Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
1532               100             105             110
1533
1534   Lys Arg
1535
1536
1537   (2) INFORMATION FOR SEQ ID NO:37:
1538
1539        (i) SEQUENCE CHARACTERISTICS:
1540             (A) LENGTH: 327 base pairs
1541             (B) TYPE: nucleic acid
1542             (C) STRANDEDNESS: both
1543             (D) TOPOLOGY: linear
1544
1545       (ii) MOLECULE TYPE: cDNA
1546
1547      (iii) HYPOTHETICAL: NO
1548
1549       (iv) ANTI-SENSE: NO
1550
1551
1552       (ix) FEATURE:
1553             (A) NAME/KEY: CDS
1554             (B) LOCATION: 1..327
1555
1556
1557       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
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1559   GCC CTC GTG ATG ACC CAG ACT CCA GCC TCC GTG TCT GCA GCT GTG GGA      48
1560   Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1561    1               5               10              15
1562
1563   GGC ACA GTC ACC ATC AAG TGC CAG GCC AGT GAG AAC ATT TAC AGC TCT      96
1564   Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Asn Ile Tyr Ser Ser
1565           20              25              30
1566
1567   TTA GCC TGG TAT CAG CAG AAA CCA GGG CAG CCT CCC AAG CTC CTG ATC     144
1568   Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1569           35              40              45
1570
1571   TAT GGT GCA TCC ACT CTG GCA TCT GGG GTC CCA TCG CGG TTC AAA GGC     192
1572   Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
1573           50              55              60
1574
1575   AGT AGA TCT GGG ACA GAG TAC ACT CTC ACC ATC AGC GGC GTG CAG CGT     240
1576   Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg
1577    65              70              75              80
1578
1579   GAG GAT GCT GCC ACC TAC TAC TGT CTA GGC AGT GAT AGT AGT AGC GAT     288
1580   Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Asp Ser Ser Ser Asp
1581           85              90              95
```

```
1582
1583    ACT GCT TTC GGC GGA GGG ACC GAG CTG GAG ATC CTA TGT          327
1584    Thr Ala Phe Gly Gly Gly Thr Glu Leu Glu Ile Leu Cys
1585                100                 105
1586
1587
1588    (2) INFORMATION FOR SEQ ID NO:38:
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1590          (i) SEQUENCE CHARACTERISTICS:
1591                (A) LENGTH: 109 amino acids
1592                (B) TYPE: amino acid
1593                (D) TOPOLOGY: linear
1594
1595          (ii) MOLECULE TYPE: protein
1596
1597          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
1598
1599    Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1600     1               5                 10                 15
1601
1602    Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Asn Ile Tyr Ser Ser
1603                20                 25                 30
1604
1605    Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1606                35                 40                 45
1607
1608    Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
1609          50                 55                 60
1610
1611    Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg
1612     65                 70                 75                 80
1613
1614    Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Asp Ser Ser Ser Asp
1615                85                 90                 95
1616
1617    Thr Ala Phe Gly Gly Gly Thr Glu Leu Glu Ile Leu Cys
1618                100                 105
1619
1620    (2) INFORMATION FOR SEQ ID NO:39:
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1622          (i) SEQUENCE CHARACTERISTICS:
1623                (A) LENGTH: 321 base pairs
1624                (B) TYPE: nucleic acid
1625                (C) STRANDEDNESS: both
1626                (D) TOPOLOGY: linear
1627
1628          (ii) MOLECULE TYPE: cDNA
1629
1630          (iii) HYPOTHETICAL: NO
1631
1632          (iv) ANTI-SENSE: NO
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1634
1635        (ix)  FEATURE:
1636              (A)  NAME/KEY: CDS
1637              (B)  LOCATION: 1..321
1638
1639
1640        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:39:
1641
1642   ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG         48
1643   Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1644    1               5                  10                  15
1645
1646   TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT         96
1647   Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1648               20                  25                  30
1649
1650   CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG        144
1651   Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
1652               35                  40                  45
1653
1654   GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC        192
1655   Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
1656           50                  55                  60
1657
1658   TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA        240
1659   Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
1660   65                  70                  75                  80
1661
1662   CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC        288
1663   His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1664               85                  90                  95
1665
1666   GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG                            321
1667   Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1668               100                 105
1669
1670
1671      (2)  INFORMATION FOR SEQ ID NO:40:
1672
1673           (i)  SEQUENCE CHARACTERISTICS:
1674               (A)  LENGTH: 106 amino acids
1675               (B)  TYPE: amino acid
1676               (D)  TOPOLOGY: linear
1677
1678           (ii)  MOLECULE TYPE: protein
1679
1680           (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:40:
1681
1682   Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1683    1               5                  10                  15
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DATE: 07/29/93
TIME: 14:50:05

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1685    Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1686                20                  25                  30
1687
1688    Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
1689                35                  40                  45
1690
1691    Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
1692            50                  55                  60
1693
1694    Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
1695    65                  70                  75                  80
1696
1697    His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1698                85                  90                  95
1699
1700    Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1701                100                 105
1702
1703
1704    (2)  INFORMATION FOR SEQ ID NO:41:
1705
1706         (i)  SEQUENCE CHARACTERISTICS:
1707              (A)  LENGTH: 321 base pairs
1708              (B)  TYPE: nucleic acid
1709              (C)  STRANDEDNESS: both
1710              (D)  TOPOLOGY: linear
1711
1712        (ii)  MOLECULE TYPE: cDNA
1713
1714       (iii)  HYPOTHETICAL: YES
1715
1716        (iv)  ANTI-SENSE: NO
1717
1718
1719        (ix)  FEATURE:
1720              (A)  NAME/KEY: CDS
1721              (B)  LOCATION: 1..321
1722
1723
1724        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:41:
1725
1726    GCT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAG GAT CAG        48
1727    Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln
1728     1               5                  10                  15
1729
1730    GTG AAA TCT GGA ACT GTC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT        96
1731    Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1732                20                  25                  30
1733
1734    CCC AGA GAG GCC AGC GTA AAG TGG AAG GTG GAT GGT GCC CTC AAA ACG       144
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1735      Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
1736              35                  40                  45
1737
1738      GAT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AAC ACC        192
1739      Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
1740          50                  55                  60
1741
1742      TAC AGC CTG AGC AGC ACC CTG ACG CTG AGC AGC ACA GAC TAC CAG AGT        240
1743      Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
1744      65                  70                  75                  80
1745
1746      CAC AAT GTC TAT GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC        288
1747      His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1748                  85                  90                  95
1749
1750      GTC ACC AAG AGC TTC AAC AGG GGA GAG TGT TAG                           321
1751      Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1752              100                 105
1753
1754
1755      (2)  INFORMATION FOR SEQ ID NO:42:
1756
1757          (i)  SEQUENCE CHARACTERISTICS:
1758              (A)  LENGTH: 106 amino acids
1759              (B)  TYPE: amino acid
1760              (D)  TOPOLOGY: linear
1761
1762          (ii)  MOLECULE TYPE: protein
1763
1764          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:42:
1765
1766      Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln
1767      1               5                   10                  15
1768
1769      Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1770              20                  25                  30
1771
1772      Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
1773              35                  40                  45
1774
1775      Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
1776          50                  55                  60
1777
1778      Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
1779      65                  70                  75                  80
1780
1781      His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1782                  85                  90                  95
1783
1784      Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1785              100                 105
```

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1786
1787
1788      (2) INFORMATION FOR SEQ ID NO:43:
1789
1790          (i) SEQUENCE CHARACTERISTICS:
1791              (A) LENGTH: 321 base pairs
1792              (B) TYPE: nucleic acid
1793              (C) STRANDEDNESS: both
1794              (D) TOPOLOGY: linear
1795
1796         (ii) MOLECULE TYPE: cDNA
1797
1798        (iii) HYPOTHETICAL: NO
1799
1800         (iv) ANTI-SENSE: NO
1801
1802
1803         (ix) FEATURE:
1804              (A) NAME/KEY: CDS
1805              (B) LOCATION: 1..321
1806
1807
1808         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
1809
1810      GAT CCA ATT GCG CCT ACT GTC CTC CTC TTC CCA CCA TCT GCT GAT CAG      48
1811      Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln
1812       1               5                  10                  15
1813
1814      CTG ACA ACT GAA ACA GTC ACC ATC GTG TGC GTG GCA AAT AAA TTC CGT      96
1815      Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg
1816                   20                  25                  30
1817
1818      CCC AAT GAC ATC ACC GTC ACC TGG AAG GTG GAT GAC GAA ATC CAA CAG     144
1819      Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln
1820                   35                  40                  45
1821
1822      AGC GGC TTC GAG AAC AGT ACA ACA CCG CAG AGC CCC GAG GAC TGT ACC     192
1823      Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr
1824           50                  55                  60
1825
1826      TAC AAC CTC AGC AGC ACT CTG TCA CTG ACC AAA GCA CAG TAC AAC AGC     240
1827      Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser
1828       65                  70                  75                  80
1829
1830      CAC AGC GTG TAC ACC TGC GAG GTG GTC CAT CAC AAC TCG GGC TCA GCG     288
1831      His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala
1832                   85                  90                  95
1833
1834      ATC GTC CAG AGC TTC AAT AGG GGT GAC TGT TAG                         321
1835      Ile Val Gln Ser Phe Asn Arg Gly Asp Cys
1836                  100                 105
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INPUT SET: S1104.raw

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1837
1838
1839      (2)  INFORMATION FOR SEQ ID NO:44:
1840
1841           (i)  SEQUENCE CHARACTERISTICS:
1842                    (A)  LENGTH: 106 amino acids
1843                    (B)  TYPE: amino acid
1844                    (D)  TOPOLOGY: linear
1845
1846          (ii)  MOLECULE TYPE: protein
1847
1848          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:44:
1849
1850      Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln
1851       1               5                  10                  15
1852
1853      Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg
1854                   20              25                  30
1855
1856      Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln
1857           35                  40                  45
1858
1859      Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr
1860           50                  55                  60
1861
1862      Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser
1863       65                  70                  75                  80
1864
1865      His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala
1866                   85                  90                  95
1867
1868      Ile Val Gln Ser Phe Asn Arg Gly Asp Cys
1869                  100                 105
1870
1871
1872
1873      (2)  INFORMATION FOR SEQ ID NO:45:
1874
1875           (i)  SEQUENCE CHARACTERISTICS:
1876                    (A)  LENGTH: 321 base pairs
1877                    (B)  TYPE: nucleic acid
1878                    (C)  STRANDEDNESS: both
1879                    (D)  TOPOLOGY: linear
1880
1881          (ii)  MOLECULE TYPE: cDNA
1882
1883         (iii)  HYPOTHETICAL: NO
1884
1885          (iv)  ANTI-SENSE: NO
1886
1887
```

```
1888          (ix)  FEATURE:
1889                     (A)  NAME/KEY: CDS
1890                     (B)  LOCATION: 1..321
1891
1892
1893          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:45:
1894
1895     GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT GAG CAG        48
1896     Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
1897      1               5                  10                  15
1898
1899     TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC TTC TTG AAC AAC TTC TAC        96
1900     Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
1901              20                  25                  30
1902
1903     CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT GAT GGC AGT GAA CGA CAA       144
1904     Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
1905              35                  40                  45
1906
1907     AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG GAC AGC AAA GAC AGC ACC       192
1908     Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
1909              50                  55                  60
1910
1911     TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC AAG GAC GAG TAT GAA CGA       240
1912     Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
1913      65                  70                  75                  80
1914
1915     CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC AAG ACA TCA ACT TCA CCC       288
1916     His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
1917                      85                  90                  95
1918
1919     ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT TAG                           321
1920     Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
1921                     100                 105
1922
1923
1924      (2)  INFORMATION FOR SEQ ID NO:46:
1925
1926           (i)  SEQUENCE CHARACTERISTICS:
1927                     (A)  LENGTH: 106 amino acids
1928                     (B)  TYPE: amino acid
1929                     (D)  TOPOLOGY: linear
1930
1931           (ii)  MOLECULE TYPE: protein
1932
1933           (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:46:
1934
1935     Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
1936      1               5                  10                  15
1937
1938     Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
```

INPUT SET: S1104.raw

```
1939                  20                      25                      30
1940
1941   Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
1942           35                      40                      45
1943
1944   Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
1945           50                      55                      60
1946
1947   Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
1948       65                      70                      75                      80
1949
1950   His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
1951                   85                      90                      95
1952
1953   Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
1954               100                     105
1955
1956
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1104.raw

Line	Error	Original Text		
27	Wrong application Serial Number	(A) APPLICATION NUMBER: US 07/952640		
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
591	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:		
10	Number of Sequences Doesn't Equal Actual	(iii) NUMBER OF SEQUENCES: 46		

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1104.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/07/952,640A*

INPUT SET: S1104.raw

Line	Original Text	Corrected Text
1262	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
1285	(2) INFORMATION FOR SEQ ID NO:31	(2) INFORMATION FOR SEQ ID NO:31:
1305	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
1336	(2) INFORMATION FOR SEQ ID NO:32	(2) INFORMATION FOR SEQ ID NO:32:
1345	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
1368	(2) INFORMATION FOR SEQ ID NO:33	(2) INFORMATION FOR SEQ ID NO:33:
1388	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
1419	(2) INFORMATION FOR SEQ ID NO:34	(2) INFORMATION FOR SEQ ID NO:34:
1428	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1112.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: US 07/952640

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1112.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1112.raw

Line	Original Text	Corrected Text
1264	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
1287	(2) INFORMATION FOR SEQ ID NO:31	(2) INFORMATION FOR SEQ ID NO:31:
1307	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
1338	(2) INFORMATION FOR SEQ ID NO:32	(2) INFORMATION FOR SEQ ID NO:32:
1347	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
1370	(2) INFORMATION FOR SEQ ID NO:33	(2) INFORMATION FOR SEQ ID NO:33:
1390	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
1421	(2) INFORMATION FOR SEQ ID NO:34	(2) INFORMATION FOR SEQ ID NO:34:
1430	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: